Appendix III

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23°C during daylight hours (15h) and dropped to 15°C at night. Foliage blight scores were
recorded 69, 92, 116, and 163 hours after inoculation. A blight scale, with 0 indicating a dead
plant and 9 no visible infection, was used to visually rate disease severity. All the plants were
tested in three repetitions. The ratings and the ranges of percentage infections associated with

5 the rating value were as follows: 9, no visible infection; 8, less than 10% infection; 7, 11-25%
infection; 6, 26-40% infection; 5, 41 to 60% infection; 4, 61-70% infection; 3, 71-80% infection;
2, 81-90% infection; 1, greater than 90% infection; 0, all dead. Plants with scores of 8 or above
were scored as resistant and plants with scores of 6.9 or below were scored as susceptible. Plants
with scores between 6.9 and 8 were scored as intermediate resistant.

10   Transgenic plants with gene 2 were tested using the above method. 69, 92, 116, and 163
hours after inoculation, the average resistant score for transgenic plants with gene 2 was 7.3.

Example 5:

      The following example shows an amino acid comparison between the gene 2 coding
15 region from a disease resistant and disease susceptible variety. The top sequence is the gene 2
coding region from the susceptible 177013 homolog. The bottom sequence is the gene 2 coding
region from the resistant homolog. Note that on the line numbered 451, at residue 454, a single
nucleotide difference between R and S changes a Tyrosine (Y; resistant) to an amber stop codon.

20
        1 MAEAFTQVLLDNLTSFLKGELALLPGFQDERQRLSSMFSTIQAVLEDAQE 50
          |||||||||||||||||| |||||||||||||||||||||||||||||
        1 MAEAFTQVLLDNLTSFLKGELVLLFGFQDEFQRLSSMFSTIQAVLEDAQE 50

25   51 KQLNNKPLEWWLQKLNAATYEVDDILDEYKTKATRFSQSEYGRYHPKVIP 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
       51 KQLNNKPLEWWLQKLNAATYEVDDILDEYKTKATRFSQSEYGRYHPKVIP 100

30   101 FRHKVGKRMDQVMKKLKAIAEERKNFILHEKIVERQAVRRKTGSVLTKFQ 150
          ||||||||||||||||||| ||||| |||||||||||||||||||||||
      101 FRHKVGKRMDQVMKKLKATAEERKSFKLHFKIVERQAVRRKTGSVLTKFQ 150

35   151 VYGRDKEKDEIVKILINNVSDAQHLSVLPILG4OGLGKFTLAQMVFNEQR 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      151 VYGHDKEKDEIVKFLINNVSDAQHLSVLPILGHMGLGKTTLAQMVFNEQR 200

      201 VTERFHSKIMICVSEDFDEKRLIKAIVESIEGRPLLGEMDLAPLQKLQE 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||
      201 VTEDFHSKIMTCVSEDFDEKRLIKAIVESIEGRPLLGEMDLAPLQKLQE 250

40   251 LLNGKRYLLVLDDVWNEDQQKWANLRAVLKVGASGASVLTTTRLEKVGSI 300
          |||||||||||||||||||||||||||||||||||||||||||||||||
      251 LLNGKRYLLVLDDVWNEDQQKWANLRAVLKVGASGASVLTTTRLEKVGSI 300

45   301 MGTLQFYELSNLSQEDCWLLFMQRAFGRQQEINFNLVAIGKEIVKKSGGV 350
          |||||||||||||||||||||||||||||||||||||||||||||||||
      301 MGTLQFYELSNLSQEDCWLLFMQRAFGRQQEINFRLVAIGKEIVKKSGGV 350

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351 PLAAKTLCGILCFKREERAWEHVRDSPIWNLPQDESSILPALRLSYHQLP 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 PLAAKTLGGILCFKNEERAWEHVRDSPIWNLPQDESSILPALRLSYHQLP 400

401 LDLKQCFAYCAVFFKDAKMEKFKLISNWMAHGFLLSKGHMELEDVGDEVW 450
    ||||||||||||||||||||||| ||||||||||||||||||||||||||
401 LDLKQCFAYCAVFFKDAKMEKKLLSLWAHGFLLSKGNMELEDVGDEVW 450

451 KLL*LRSFFQEIEVRDGKTYFKNHDLIHDLATSLFSANTSSSNIRENWR 500
    ||||  ||||||||||||||||||||||||||||||||||||||||||
451 KELYLRSFFQEIEVRDGKTYFKNHDLIHDLATSLFSANTSSSNIREINKR 500

501 SYTHRMNSIGFAEVVFFYTLPPLEKFISLRVLNLGDSTFWRLPSSIGDLVH 550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 SYTHRMMSIGFAEVVFFYTLPPLEKFISLRVLNLGDSTFWRLPSSIGDLVH 550

551 LRYLNLYGSGMRSLFKQLCKLQNLQTLDLIQYCTKLCCLPKETSKLGSLRN 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
551 LRYLNLYGSGMRSLFKQLCKLQNLQTLDLIQYCTKLCCLPKETSKLGSLRN 600

601 LLLDGSQSLTCMPTRIGSLTCLKTLGQFVVGRKRGYQLGELGNLNLYGSI 650
    |||||||||||||||||||||||||||||||||||||||||||||||||
601 LLLDGSQSLTCMPTRIGSLTCLKTLGQFVVGRKKGYQLGELGNLNLYGSI 650

651 KIGHLERVKNDKDAKEANLSAKGNLHSLSMSWNNFGPHIYESEEVRVLEA 700
    |||||||||| |||||||||||||||||||||||||||||||||||||||
651 KISHLERVRHDMDAKEANLSAKGNLHSLSMSWNNFGPHIYESEEVRVLEA 700

701 LKPHSNLTSLKIYGFRGIHLPEWMNHSVLKNIVSILISWFRNCSCLPPFG 750
    ||||||||||||||||||||||||||||||||||||||||||||||||||
701 LKPHSNLTSLKIYGFRGIHLPEWMNHSVLKNIVSILISWFRNCSCLPPFG 750

751 DLPCLESLELHWGSAOVEYVEEVDIDVNSGFPTRIRFPSLRKLDIWDFGS 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 DLPCLESLELHWGSADVEYVEEVDIDVNSGFPTRIRFPSLRKLDIWDFGS 800

801 LKGLLKKEGEEQFFVLEEMIIHECPFLTLSSNLRALFSLRICYNKVATSF 850
    ||||||||||||||||||||||||||||||||||||||||||||||||||
801 LKGLLKKEGEEQFFVLEEMIIHECPFLTLSSNLRALFSLRICYNKVATSF 850

851 PEEMFKNLAHLKYLTISHCNNLKELPTSLASLNALKSL......ALESLP 894
    |||||||||||||||||||||||||||||||||||||      ||||||
852 PEEMFKNLAHLKYLTISHCNNLKELPTSLASLNALKSLKIQLCCALESLP 900

895 EEGLEGLSSLTELFVEHCNPLKCLPEGLQHLTVLTSLKTRGCPQLIKRCE 944
    ||||||||||||||||||||||||||||||||||||||||||||||||||
901 EEGLEGLSSLTELFVEHCRMLKCLPEGLQHLTVLTSLKIRGCPQLIKRCE 950

945 KGIGEDWHKISHIPNVNIYI* 965
    ||||||||||||||||||||
951 KGIGEDWHKISHIPNVNIYI* 971
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<u>Example 6</u>:

The following example shows a nucleic acid comparison between the gene 2 coding regions from a disease resistant and disease susceptible variety. The top sequence is the gene 2 coding region from the resistant homolog. The bottom sequence is the gene 2 coding region

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